

Attorney Docket No: 16517  
Application No. 10/775,176  
Page 2 of 4

### CLAIM AMENDMENTS

This listing of claims will replace all prior versions, and listings, of claims in the application.

#### LISTING OF CLAIMS

RECEIVED  
CENTRAL FAX CENTER  
APR 24 2007

Claims 1-51 (Cancelled)

Claim 52 (Currently Amended) A method for gene prediction by determining a probability for each of one or more states for more than one selected nucleotide in a nucleic acid sequence comprising:

- a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in a window of a first selected nucleotide;
- b) determining transition probabilities for each of said states for nucleotides within said window following said initial oligonucleotide;
- c) using said initial oligonucleotide probability and said transition probabilities to determine a plurality of window probabilities, wherein said plurality comprises a window probability corresponding to each of said states for said selected nucleotide;
- d) applying a bias function to said plurality of window probabilities, to determine a probability for each of said states for said selected nucleotide, wherein the value produced by said bias function is at least different in one state within said bias function does not have the same value in all of said states for said selected nucleotide; and,
- e) repeating steps a) through d) for each remaining selected nucleotide in said nucleic acid sequence,

wherein said more than one selected nucleotide are contiguous, and step e) is performed sequentially from said first selected nucleotide to a last selected nucleotide,

wherein said probability for each of said states for said more than one selected nucleotide is determined using an inhomogeneous Markov model having eight states, wherein said eight states are: first reading frame positive strand (1+); second reading frame positive strand (2+); third reading frame positive strand (3+); first reading frame negative strand (1-); second reading frame negative strand (2-); third reading frame negative strand (3-); noncoding positive strand (N+); and noncoding negative strand (N-).

Attorney Docket No: 16517  
 Application No. 10/775,176  
 Page 3 of 4

wherein said probability for each of said states for said more than one selected nucleotide is determined using the equation

$$P(f|s) = \frac{\phi(f) \cdot P_f \cdot P_f(S)}{\sum_{i \in \{1+, 2+, 3+, N+, 1-, 2-, 3-, N-\}} \phi(i) \cdot P_i \cdot P_i(S)}$$

Claims 53-55 (Cancelled)

Claim 56 (Previously presented) The method of claim 52, wherein said nucleic acid sequence is part of a longer nucleic acid sequence.

Claim 57 (Previously presented) The method of claim 52, wherein each selected nucleotide in said more than one selected nucleotide is the middle nucleotide in its own window.

Claims 58-59 (Cancelled)

Claim 60 (Currently amended) The method of claim 52, wherein the value produced by said bias function is said bias function has a value between 0.0 and 0.9, or greater than 1.1, in one or more of said states for said selected nucleotide.